



SEQUENCE LISTING

<110> Cochran, Mark D
Cook, Stephanie M
Wild, Martha A

<120> Novel Avian Herpes Virus and Uses Thereof

<130> SY01105K1QKQK

<140> US 09/881,457

<141> 2001-06-14

<150> 09/426,352

<151> 1999-10-25

<150> 08/804,372

<151> 1997-02-21

<150> PCT/US95/10245

<151> 1995-08-09

<150> 08/663,566

<151> 1996-06-13

<150> 08/288,065

<151> 1994-08-09

<150> PCT/US93/05681

<151> 1993-06-14

<150> 08/023,610

<151> 1993-02-26

<150> 07/898,087

<151> 1992-06-12

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 3570

<212> DNA

<213> Newcastle disease virus

<220>

<221> CDS

<222> (1194)..(2888)

<223> NDV Fusion Protein

<220>

<221> misc feature

<222> (1355)

<223> n = any nucleotide

<400> 1

gtacgttaat taaccggga agcttgcag cctgcagtga ataataaaat gtgtgtttgt 60
ccgaaatacg cgttttgaga tttctgtcgc cgactaaatt catgtcgcgc gatagtgggtg 120
tttatcgccg atagagatgg cgatattgga aaaatcgata ttgaaaata tggcatattg 180
aaaatgtcgc cgatgtgagt ttctgtgtaa ctgatatctg gcgatagcgc ttatatcggt 240
tacgggggat ggcgatagac gactttggcg acttggggcg ttctgtgtgt cgaaatatc 300
gcagtttcga tataggtgac agacgatatg aggctatatc gccgatagag gcgacatcaa 360

gctggcacat	ggccaatgca	tatcgatcta	tacattgaat	caatattggc	aattagccat	420
attagtcatt	ggttatatag	cataaatcaa	tattggctat	tggccattgc	atacgttgta	480
tctatatcat	aatatgtaca	tttatattgg	ctcatgtcca	atatgaccgc	catgttgaca	540
ttgattattg	actagttatt	aatagtaatc	aattacgggg	tcattagttc	atagcccata	600
tatggagttc	cgcgttacat	aacttacggt	aaatggcccg	cctggctgac	cgcccaacga	660
ccccgcgcca	ttgacgtcaa	taatgacgta	tgttcccata	gtaacgccaa	tagggacttt	720
ccattgacgt	caatgggtgg	agtatttacg	gtaaaactgcc	cacttggcag	tacatcaagt	780
gtatcatatg	ccaagtcgcg	cccctattga	cgtcaatgac	ggtaaattggc	ccgcctggca	840
ttatgcccgag	tacatgacct	tacgggactt	tcctacttgg	cagtacatct	acgtattagt	900
catcgctatt	accatggtga	tgcggttttg	gcagtacacc	aatgggcgtg	gatagcggtt	960
tgactcacgg	ggattttcaa	gtctccaccc	cattgacgtc	aatgggagtt	tgttttggca	1020
ccaaaatcaa	cgggactttc	caaaatgtcg	taataacccc	gccccgttga	cgcaaattggg	1080
cggtaggcgt	gtacggtggg	aggtctatat	aagcagagct	cgttttagtga	accgtcagat	1140
cgcttgagga	cgccatccac	gctgttttga	cctccataga	agacaccggg	acc atg Met	1196

gat cga tcc cgg ttg gcg ccc tcc agg tgc agg atg ggc tcc aga cct 1244
Asp Arg Ser Arg Leu Ala Pro Ser Arg Cys Arg Met Gly Ser Arg Pro
5 10 15

tct acc aag aac cca gca cct atg atg ctg act atc cgg gtc gcg ctg 1292
Ser Thr Lys Asn Pro Ala Pro Met Met Leu Thr Ile Arg Val Ala Leu
20 25 30

gta ctg agt tgc atc tgt ccg gca aac tcc att gat ggc agg cct ctt 1340
Val Leu Ser Cys Ile Cys Pro Ala Asn Ser Ile Asp Gly Arg Pro Leu
35 40 45

gca gct gca gga ctn tgg tta cag gag aca aag caa tca aca tat aca 1388
Ala Ala Ala Gly Xaa Trp Leu Gln Glu Thr Lys Gln Ser Thr Tyr Thr
50 55 60 65

cct cat ccc aga cag gtc aat cat att aag ctc ctc ccg aat ctg cca 1436
Pro His Pro Arg Gln Val Asn His Ile Lys Leu Leu Pro Asn Leu Pro
70 75 80

aag gat aag gag gca tgt gcg aaa gcc ccc ttg gat gca tac aac agg 1484
Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro Leu Asp Ala Tyr Asn Arg
85 90 95

aca ttg acc act ttg ctc acc ccc ctt ggt gac tct atc cgt agg ata 1532
Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly Asp Ser Ile Arg Arg Ile
100 105 110

caa gag tct gtg act aca tct gga ggg ggg aga cag ggg cgc ctt ata 1580
Gln Glu Ser Val Thr Thr Ser Gly Gly Gly Arg Gln Gly Arg Leu Ile
115 120 125

ggc gcc att att ggc ggt gtg gct ctt ggg gtt gca act gcc gca caa 1628
Gly Ala Ile Ile Gly Gly Val Ala Leu Gly Val Ala Thr Ala Ala Gln
130 135 140 145

ata aca gcg gcc gca gct ctg ata caa gcc aaa caa aat gct gcc aac 1676
Ile Thr Ala Ala Ala Ala Leu Ile Gln Ala Lys Gln Asn Ala Ala Asn
150 155 160

atc ctc cga ctt aaa gag agc att gcc gca acc aat gag gct gtg cat	1724
Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala Thr Asn Glu Ala Val His	
	165 170 175
gag gtc act gac gga tta tcg caa cta gca gtg gca gtt ggg aag atg	1772
Glu Val Thr Asp Gly Leu Ser Gln Leu Ala Val Ala Val Gly Lys Met	
	180 185 190
cag cag ttc gtt aat gac caa ttt aat aaa aca gct cag gaa tta gac	1820
Gln Gln Phe Val Asn Asp Gln Phe Asn Lys Thr Ala Gln Glu Leu Asp	
	195 200 205
tgc atc aaa att gca cag caa gtt ggt gta gag ctc aac ctg tac cta	1868
Cys Ile Lys Ile Ala Gln Gln Val Gly Val Glu Leu Asn Leu Tyr Leu	
	210 215 220 225
acc gaa tcg act aca gta ttc gga cca caa atc act tca cct gcc tta	1916
Thr Glu Ser Thr Thr Val Phe Gly Pro Gln Ile Thr Ser Pro Ala Leu	
	230 235 240
aac aag ctg act att cag gca ctt tac aat cta gct ggt ggg aat atg	1964
Asn Lys Leu Thr Ile Gln Ala Leu Tyr Asn Leu Ala Gly Gly Asn Met	
	245 250 255
gat tac tta ttg act aag tta ggt ata ggg aac aat caa ctc agc tca	2012
Asp Tyr Leu Leu Thr Lys Leu Gly Ile Gly Asn Asn Gln Leu Ser Ser	
	260 265 270
tta atc ggt agc ggc tta atc acc ggt aac cct att cta tac gac tca	2060
Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn Pro Ile Leu Tyr Asp Ser	
	275 280 285
cag act caa ctc ttg ggt ata cag gta act cta cct tca gtc ggg aac	2108
Gln Thr Gln Leu Leu Gly Ile Gln Val Thr Leu Pro Ser Val Gly Asn	
	290 295 300 305
cta aat aat atg cgt gcc acc tac ttg gaa acc tta tcc gta agc aca	2156
Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu Thr Leu Ser Val Ser Thr	
	310 315 320
acc agg gga ttt gcc tcg gca ctt gtc cca aaa gtg gtg aca cgg gtc	2204
Thr Arg Gly Phe Ala Ser Ala Leu Val Pro Lys Val Val Thr Arg Val	
	325 330 335
ggt tct gtg ata gaa gaa ctt gac acc tca tac tgt ata gaa act gac	2252
Gly Ser Val Ile Glu Glu Leu Asp Thr Ser Tyr Cys Ile Glu Thr Asp	
	340 345 350
tta gat tta tat tgt aca aga ata gta acg ttc cct atg tcc cct ggt	2300
Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr Phe Pro Met Ser Pro Gly	
	355 360 365
att tac tcc tgc ttg agc ggc aat aca tcg gcc tgt atg tac tca aag	2348
Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser Ala Cys Met Tyr Ser Lys	
	370 375 380 385
acc gaa ggc gca ctt act aca cca tat atg act atc aaa ggc tca gtc	2396
Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met Thr Ile Lys Gly Ser Val	
	390 395 400
atc gct aac tgc aag atg aca aca tgt aga tgt gta aac ccc ccg ggt	2444
Ile Ala Asn Cys Lys Met Thr Thr Cys Arg Cys Val Asn Pro Pro Gly	
	405 410 415
atc ata tcg caa aac tat gga gaa gcc gtg tct cta ata gat aaa caa	2492
Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val Ser Leu Ile Asp Lys Gln	
	420 425 430

tca tgc aat gtt tta tcc tta ggc ggg ata act tta agg ctc agt ggg	2540
Ser Cys Asn Val Leu Ser Leu Gly Gly Ile Thr Leu Arg Leu Ser Gly	
435 440 445	
gaa ttc gat gta act tat cag aag aat atc tca ata caa gat tct caa	2588
Glu Phe Asp Val Thr Tyr Gln Lys Asn Ile Ser Ile Gln Asp Ser Gln	
450 455 460 465	
gta ata ata aca ggc aat ctt gat atc tca act gag ctt ggg aat gtc	2636
Val Ile Ile Thr Gly Asn Leu Asp Ile Ser Thr Glu Leu Gly Asn Val	
470 475 480	
aac aac tcg atc agt aat gcc ttg aat aag tta gag gaa agc aac aga	2684
Asn Asn Ser Ile Ser Asn Ala Leu Asn Lys Leu Glu Glu Ser Asn Arg	
485 490 495	
aaa cta gac aaa gtc aat gtc aaa ctg acc agc aca tct gct ctc att	2732
Lys Leu Asp Lys Val Asn Val Lys Leu Thr Ser Thr Ser Ala Leu Ile	
500 505 510	
acc tat atc gtt ttg act atc ata tct ctt gtt ttt ggt ata ctt agc	2780
Thr Tyr Ile Val Leu Thr Ile Ile Ser Leu Val Phe Gly Ile Leu Ser	
515 520 525	
ctg att cta gca tgc tac cta atg tac aag caa aag gcg caa caa aag	2828
Leu Ile Leu Ala Cys Tyr Leu Met Tyr Lys Gln Lys Ala Gln Gln Lys	
530 535 540 545	
acc tta tta tgg ctt ggg aat aat acc cta gat cag atg aga gcc act	2876
Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu Asp Gln Met Arg Ala Thr	
550 555 560	
aca aaa atg tga acacagatga ggaacgaagg tttccctaata agtaatttgt	2928
Thr Lys Met	

gtgaaagtgc tggtagtctg tcagttcgga gagttaagaa aaaaaaaaaa ccccccccc	2988
cccccccccc cccccctggg tacgatcctc tagagtcggg agatggggga ggctaactga	3048
aacacggaag gagacaatac cggaaggaaac ccgcgctatg acggcaataa aaagacagaa	3108
taaaacgcac ggggtgttggg tcgtttgttc ataaacgcgg ggttcgggtcc cagggctggc	3168
actctgtcga taccaccacg agacccatt gggaccaata cgcgcggtt tcttcctttt	3228
ccccccccca acccccaagt tcgggtgaag gcccagggtc cgcagccaac gtcggggcgg	3288
caagccctgc catagccacg ggccccgtgg gttagggacg gggccccca tggggaatgg	3348
tttatgggtc gtgggggtta ttattttggg cgttgcgtgg ggtcagggtcc acgactggac	3408
tgagcagaca gaccatggt ttttgatgg cctgggcatg gaccgcatgt actggcgca	3468
cacgaacacc gggcgtctgt ggctgcaaaa ccccccgac ccccaaaaac caccgcgcg	3528
atttctggcg ccgccggacg tcgacttaat taacaagctt ag	3570

<210> 2
 <211> 564
 <212> PRT
 <213> Newcastle disease virus

<220>
 <221> misc_feature
 <222> (54)
 <223> Xaa = any amino acid

<400> 2

Met	Asp	Arg	Ser	Arg	Leu	Ala	Pro	Ser	Arg	Cys	Arg	Met	Gly	Ser	Arg
1				5					10					15	
Pro	Ser	Thr	Lys	Asn	Pro	Ala	Pro	Met	Met	Leu	Thr	Ile	Arg	Val	Ala
			20					25					30		
Leu	Val	Leu	Ser	Cys	Ile	Cys	Pro	Ala	Asn	Ser	Ile	Asp	Gly	Arg	Pro
		35					40					45			
Leu	Ala	Ala	Ala	Gly	Xaa	Trp	Leu	Gln	Glu	Thr	Lys	Gln	Ser	Thr	Tyr
	50					55					60				
Thr	Pro	His	Pro	Arg	Gln	Val	Asn	His	Ile	Lys	Leu	Leu	Pro	Asn	Leu
	65				70					75					80
Pro	Lys	Asp	Lys	Glu	Ala	Cys	Ala	Lys	Ala	Pro	Leu	Asp	Ala	Tyr	Asn
				85					90					95	
Arg	Thr	Leu	Thr	Thr	Leu	Leu	Thr	Pro	Leu	Gly	Asp	Ser	Ile	Arg	Arg
			100					105					110		
Ile	Gln	Glu	Ser	Val	Thr	Thr	Ser	Gly	Gly	Gly	Arg	Gln	Gly	Arg	Leu
		115					120					125			
Ile	Gly	Ala	Ile	Ile	Gly	Gly	Val	Ala	Leu	Gly	Val	Ala	Thr	Ala	Ala
	130					135					140				
Gln	Ile	Thr	Ala	Ala	Ala	Ala	Leu	Ile	Gln	Ala	Lys	Gln	Asn	Ala	Ala
	145				150					155					160
Asn	Ile	Leu	Arg	Leu	Lys	Glu	Ser	Ile	Ala	Ala	Thr	Asn	Glu	Ala	Val
				165					170					175	
His	Glu	Val	Thr	Asp	Gly	Leu	Ser	Gln	Leu	Ala	Val	Ala	Val	Gly	Lys
			180					185					190		
Met	Gln	Gln	Phe	Val	Asn	Asp	Gln	Phe	Asn	Lys	Thr	Ala	Gln	Glu	Leu
		195					200					205			
Asp	Cys	Ile	Lys	Ile	Ala	Gln	Gln	Val	Gly	Val	Glu	Leu	Asn	Leu	Tyr
	210					215					220				
Leu	Thr	Glu	Ser	Thr	Thr	Val	Phe	Gly	Pro	Gln	Ile	Thr	Ser	Pro	Ala
	225				230					235					240
Leu	Asn	Lys	Leu	Thr	Ile	Gln	Ala	Leu	Tyr	Asn	Leu	Ala	Gly	Gly	Asn
			245						250					255	
Met	Asp	Tyr	Leu	Leu	Thr	Lys	Leu	Gly	Ile	Gly	Asn	Asn	Gln	Leu	Ser
			260					265					270		
Ser	Leu	Ile	Gly	Ser	Gly	Leu	Ile	Thr	Gly	Asn	Pro	Ile	Leu	Tyr	Asp
		275					280					285			
Ser	Gln	Thr	Gln	Leu	Leu	Gly	Ile	Gln	Val	Thr	Leu	Pro	Ser	Val	Gly
		290				295					300				
Asn	Leu	Asn	Asn	Met	Arg	Ala	Thr	Tyr	Leu	Glu	Thr	Leu	Ser	Val	Ser
	305				310					315					320
Thr	Thr	Arg	Gly	Phe	Ala	Ser	Ala	Leu	Val	Pro	Lys	Val	Val	Thr	Arg
				325					330					335	
Val	Gly	Ser	Val	Ile	Glu	Glu	Leu	Asp	Thr	Ser	Tyr	Cys	Ile	Glu	Thr
			340					345					350		
Asp	Leu	Asp	Leu	Tyr	Cys	Thr	Arg	Ile	Val	Thr	Phe	Pro	Met	Ser	Pro
		355					360					365			

Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser Ala Cys Met Tyr Ser
 370 375 380
 Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met Thr Ile Lys Gly Ser
 385 390 395 400
 Val Ile Ala Asn Cys Lys Met Thr Thr Cys Arg Cys Val Asn Pro Pro
 405 410 415
 Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val Ser Leu Ile Asp Lys
 420 425 430
 Gln Ser Cys Asn Val Leu Ser Leu Gly Gly Ile Thr Leu Arg Leu Ser
 435 440 445
 Gly Glu Phe Asp Val Thr Tyr Gln Lys Asn Ile Ser Ile Gln Asp Ser
 450 455 460
 Gln Val Ile Ile Thr Gly Asn Leu Asp Ile Ser Thr Glu Leu Gly Asn
 465 470 475 480
 Val Asn Asn Ser Ile Ser Asn Ala Leu Asn Lys Leu Glu Glu Ser Asn
 485 490 495
 Arg Lys Leu Asp Lys Val Asn Val Lys Leu Thr Ser Thr Ser Ala Leu
 500 505 510
 Ile Thr Tyr Ile Val Leu Thr Ile Ile Ser Leu Val Phe Gly Ile Leu
 515 520 525
 Ser Leu Ile Leu Ala Cys Tyr Leu Met Tyr Lys Gln Lys Ala Gln Gln
 530 535 540
 Lys Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu Asp Gln Met Arg Ala
 545 550 555 560
 Thr Thr Lys Met

<210> 3
 <211> 3605
 <212> DNA
 <213> Infectious Laryngotracheitis Virus

<220>
 <221> CDS
 <222> (585)..(1889)
 <223> ILTV glycoprotein D

<220>
 <221> CDS
 <222> (1997)..(3085)
 <223> ILTV glycoprotein I

<400> 3
 ctaagcttgt taattaagtc gacggcagag tcgcagacgc ccctattgga cgtcaaaatt 60
 gtagaggtga agttttcaaa cgatggcgaa gtaacggcga cttgcgtttc caccgtcaaa 120
 tctccctata gggtagaaac taattggaaa gtagacctcg tagatgtaat ggatgaaatt 180
 tctgggaaca gtcccgccgg ggtttttaac agtaatgaga aatggcagaa acagctgtac 240
 tacagagtaa ccgatggaag aacatcggtc cagctaattgt gcctgtcgtg cagagccat 300
 tctccggaac cttactgtct ttctgcacag tctcttatag cgagggaaaa agatatcgcg 360

ccagagtttat acttttacctc tgatccgcaa acggcatact gcacaataac tctgccgtcc															420		
ggcgtttgttc cgagattcga atggagcctt aataatgttt cactgccgga atatttgacg															480		
gccacgaccg ttgttttcgca taccgctggc caaagtacag tgtggaagag cagcgcgaga															540		
gcagggcgagg cgtggatttc tggccgggga ggcaatatat acga atg cac cgt cct															596		
Met His Arg Pro																	
1																	
cat	ctc	aga	cgg	cac	tcg	cgt	tac	tac	gcg	aaa	gga	gag	gtg	ctt	aac		644
His	Leu	Arg	Arg	His	Ser	Arg	Tyr	Tyr	Ala	Lys	Gly	Glu	Val	Leu	Asn		
5 10 15 20																	
aaa cac atg gat tgc ggt gga aaa cgg tgc tgc tca ggc gca gct gta															692		
Lys	His	Met	Asp	Cys	Gly	Gly	Lys	Arg	Cys	Cys	Ser	Gly	Ala	Ala	Val		
25 30 35																	
ttc act ctt ttc tgg act tgt gtc agg att atg cgg gag cat atc tgc															740		
Phe	Thr	Leu	Phe	Trp	Thr	Cys	Val	Arg	Ile	Met	Arg	Glu	His	Ile	Cys		
40 45 50																	
ttt gta cgc aac gct atg gac cgc cat tta ttt ttg agg aat gct ttt															788		
Phe	Val	Arg	Asn	Ala	Met	Asp	Arg	His	Leu	Phe	Leu	Arg	Asn	Ala	Phe		
55 60 65																	
tgg act atc gta ctg ctt tct tcc ttc gct agc cag agc acc gcc gcc															836		
Trp	Thr	Ile	Val	Leu	Leu	Ser	Ser	Phe	Ala	Ser	Gln	Ser	Thr	Ala	Ala		
70 75 80																	
gtc acg tac gac tac att tta ggc cgt cgc gcg ctc gac gcg cta acc															884		
Val	Thr	Tyr	Asp	Tyr	Ile	Leu	Gly	Arg	Arg	Ala	Leu	Asp	Ala	Leu	Thr		
85 90 95 100																	
ata ccg gcg gtt ggc ccg tat aac aga tac ctc act agg gta tca aga															932		
Ile	Pro	Ala	Val	Gly	Pro	Tyr	Asn	Arg	Tyr	Leu	Thr	Arg	Val	Ser	Arg		
105 110 115																	
ggc tgc gac gtt gtc gag ctc aac ccg att tct aac gtg gac gac atg															980		
Gly	Cys	Asp	Val	Val	Glu	Leu	Asn	Pro	Ile	Ser	Asn	Val	Asp	Asp	Met		
120 125 130																	
ata tcg gcg gcc aaa gaa aaa gag aag ggg ggc cct ttc gag gcc tcc															1028		
Ile	Ser	Ala	Ala	Lys	Glu	Lys	Glu	Lys	Gly	Gly	Pro	Phe	Glu	Ala	Ser		
135 140 145																	
gtc gtc tgg ttc tac gtg att aag ggc gac gac ggc gag gac aag tac															1076		
Val	Val	Trp	Phe	Tyr	Val	Ile	Lys	Gly	Asp	Asp	Gly	Glu	Asp	Lys	Tyr		
150 155 160																	
tgt cca atc tat aga aaa gag tac agg gaa tgt ggc gac gta caa ctg															1124		
Cys	Pro	Ile	Tyr	Arg	Lys	Glu	Tyr	Arg	Glu	Cys	Gly	Asp	Val	Gln	Leu		
165 170 175 180																	
cta tct gaa tgc gcc gtt caa tct gca cag atg tgg gca gtg gac tat															1172		
Leu	Ser	Glu	Cys	Ala	Val	Gln	Ser	Ala	Gln	Met	Trp	Ala	Val	Asp	Tyr		
185 190 195																	
gtt cct agc acc ctt gta tcg cga aat ggc gcg gga ctg act ata ttc															1220		
Val	Pro	Ser	Thr	Leu	Val	Ser	Arg	Asn	Gly	Ala	Gly	Leu	Thr	Ile	Phe		
200 205 210																	
tcc ccc act gct gcg ctc tct ggc caa tac ttg ctg acc ctg aaa atc															1268		
Ser	Pro	Thr	Ala	Ala	Leu	Ser	Gly	Gln	Tyr	Leu	Leu	Thr	Leu	Lys	Ile		
215 220 225																	
ggg aga ttt gcg caa aca gct ctc gta act cta gaa gtt aac gat cgc															1316		
Gly	Arg	Phe	Ala	Gln	Thr	Ala	Leu	Val	Thr	Leu	Glu	Val	Asn	Asp	Arg		
230 235 240																	

tgt tta aag atc ggg tcg cag ctt aac ttt tta ccg tcg aaa tgc tgg	1364
Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro Ser Lys Cys Trp	
245 250 255 260	
aca aca gaa cag tat cag act gga ttt caa ggc gaa cac ctt tat ccg	1412
Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu His Leu Tyr Pro	
265 270 275	
atc gca gac acc aat aca cga cac gcg gac gac gta tat cgg gga tac	1460
Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val Tyr Arg Gly Tyr	
280 285 290	
gaa gat att ctg cag cgc tgg aat aat ttg ctg agg aaa aag aat cct	1508
Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg Lys Lys Asn Pro	
295 300 305	
agc gcg cca gac cct cgt cca gat agc gtc ccg caa gaa att ccc gct	1556
Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln Glu Ile Pro Ala	
310 315 320	
gta acc aag aaa gcg gaa ggg cgc acc ccg gac gca gaa agc agc gaa	1604
Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala Glu Ser Ser Glu	
325 330 335 340	
aag aag gcc cct cca gaa gac tcg gag gac gac atg cag gca gag gct	1652
Lys Lys Ala Pro Glu Asp Ser Glu Asp Asp Met Gln Ala Glu Ala	
345 350 355	
tct gga gaa aat cct gcc gcc ctc ccc gaa gac gac gaa gtc ccc gag	1700
Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp Glu Val Pro Glu	
360 365 370	
gac acc gag cac gat gat cca aac tcg gat cct gac tat tac aat gac	1748
Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp Tyr Tyr Asn Asp	
375 380 385	
atg ccc gcc gtg atc ccg gtg gag gag act act aaa agt tct aat gcc	1796
Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys Ser Ser Asn Ala	
390 395 400	
gtc tcc atg ccc ata ttc gcg gcg ttc gta gcc tgc gcg gtc gcg ctc	1844
Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys Ala Val Ala Leu	
405 410 415 420	
gtg ggg cta ctg gtt tgg agc atc gta aaa tgc gcg cgt agc taa	1889
Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala Arg Ser	
425 430	
tcgagcctag aataggtggt ttcttcctac atgccacgcc tcacgctcat aatataaatc	1949
acatggaata gcataccaat gcctattcat tgggacgttc gaaaagc atg gca tcg	2005
Met Ala Ser	
435	
cta ctt gga act ctg gct ctc ctt gcc gcg acg ctc gca ccc ttc ggc	2053
Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala Pro Phe Gly	
440 445 450	
gcg atg gga atc gtg atc act gga aat cac gtc tcc gcc agg att gac	2101
Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala Arg Ile Asp	
455 460 465	
gac gat cac atc gtg atc gtc gcg cct cgc ccc gaa gct aca att caa	2149
Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala Thr Ile Gln	
470 475 480 485	
ctg cag cta ttt ttc atg cct ggc cag aga ccc cac aaa ccc tac tca	2197
Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys Pro Tyr Ser	

				490				495				500				
gga Gly	acc Thr	gtc Val	cgc Arg 505	gtc Val	gcg Ala	ttt Phe	cgg Arg	tct Ser 510	gat Asp	ata Ile	aca Thr	aac Asn	cag Gln 515	tgc Cys	tac Tyr	2245
cag Gln	gaa Glu	ctt Leu 520	agc Ser	gag Glu	gag Glu	cgc Arg	ttt Phe 525	gaa Glu	aat Asn	tgc Cys	act Thr	cat His 530	cga Arg	tcg Ser	tct Ser	2293
tct Ser	gtt Val 535	ttt Phe	gtc Val	ggc Gly	tgt Cys	aaa Lys 540	gtg Val	acc Thr	gag Glu	tac Tyr	acg Thr 545	ttc Phe	tcc Ser	gcc Ala	tcg Ser	2341
aac Asn 550	aga Arg	cta Leu	acc Thr	gga Gly	cct Pro 555	cca Pro	cac His	ccg Pro	ttt Phe	aag Lys 560	ctc Leu	act Thr	ata Ile	cga Arg	aat Asn 565	2389
cct Pro	cgt Arg	ccg Pro	aac Asn	gac Asp 570	agc Ser	ggg Gly	atg Met	ttc Phe	tac Tyr 575	gta Val	att Ile	gtt Val	cgg Arg	cta Leu 580	gac Asp	2437
gac Asp	acc Thr	aaa Lys	gaa Glu 585	ccc Pro	att Ile	gac Asp	gtc Val	ttc Phe 590	gcg Ala	atc Ile	caa Gln	cta Leu	tcg Ser 595	gtg Val	tat Tyr	2485
caa Gln	ttc Phe	gcg Ala 600	aac Asn	acc Thr	gcc Ala	gcg Ala	act Thr 605	cgc Arg	gga Gly	ctc Leu	tat Tyr	tcc Ser 610	aag Lys	gct Ala	tcg Ser	2533
tgt Cys	cgc Arg 615	acc Thr	ttc Phe	gga Gly	tta Leu	cct Pro 620	acc Thr	gtc Val	caa Gln	ctt Leu	gag Glu 625	gcc Ala	tat Tyr	ctc Leu	agg Arg	2581
acc Thr 630	gag Glu	gaa Glu	agt Ser	tgg Trp	cgc Arg 635	aac Asn	tgg Trp	caa Gln	gcg Ala	tac Tyr 640	gtt Val	gcc Ala	acg Thr	gag Glu	gcc Ala 645	2629
acg Thr	acg Thr	acc Thr	agc Ser	gcc Ala 650	gag Glu	gcg Ala	aca Thr	acc Thr	ccg Pro 655	acg Thr	ccc Pro	gtc Val	act Thr	gca Ala 660	acc Thr	2677
agc Ser	gcc Ala	tcc Ser	gaa Glu 665	ctt Leu	gaa Glu	gcg Ala	gaa Glu	cac His 670	ttt Phe	acc Thr	ttt Phe	ccc Pro	tgg Trp 675	cta Leu	gaa Glu	2725
aat Asn	ggc Gly	gtg Val 680	gat Asp	cat His	tac Tyr	gaa Glu	ccg Pro 685	aca Thr	ccc Pro	gca Ala	aac Asn	gaa Glu 690	aat Asn	tca Ser	aac Asn	2773
gtt Val	act Thr 695	gtc Val	cgt Arg	ctc Leu	ggg Gly	aca Thr 700	atg Met	agc Ser	cct Pro	acg Thr	cta Leu 705	att Ile	ggg Gly	gta Val	acc Thr	2821
gtg Val 710	gct Ala	gcc Ala	gtc Val	gtg Val	agc Ser 715	gca Ala	acg Thr	atc Ile	ggc Gly	ctc Leu 720	gtc Val	att Ile	gta Val	att Ile	tcc Ser 725	2869
atc Ile	gtc Val	acc Thr	aga Arg	aac Asn 730	atg Met	tgc Cys	acc Thr	ccg Pro	cac His 735	cga Arg	aaa Lys	tta Leu	gac Asp	acg Thr 740	gtc Val	2917
tcg Ser	caa Gln	gac Asp	gac Asp 745	gaa Glu	gaa Glu	cgt Arg	tcc Ser	caa Gln 750	act Thr	aga Arg	agg Arg	gaa Glu	tcg Ser 755	cga Arg	aaa Lys	2965
ttt Phe	gga Gly	ccc Pro 760	atg Met	gtt Val	gcg Ala	tgc Cys	gaa Glu 765	ata Ile	aac Asn	aag Lys	ggg Gly	gct Ala 770	gac Asp	cag Gln	gat Asp	3013

```

agt gaa ctt gtg gaa ctg gtt gcg att gtt aac ccg tct gcg cta agc    3061
Ser Glu Leu Val Glu Leu Val Ala Ile Val Asn Pro Ser Ala Leu Ser
      775                      780                      785

```

tcg ccc gac tca ata aaa atg tga ttaagtctga atgtggctct ccaatcattt 3115
Ser Pro Asp Ser Ile Lys Met
790 795

cgattctcta	atctcccaat	cctctcaaaa	ggggcagtat	cggacacgga	ctgggagggg	3175
cgtacacgat	agttatatgg	tacagcagag	gcctctgaac	acttaggagg	agaattcagc	3235
cggggagagc	ccctgttgag	taggcttggg	agcatattgc	aggatgaaca	tgttagtgat	3295
agttctcgcc	tcttgtcttg	cgcgctaac	ttttgcgacg	cgacacgtcc	tctttttgga	3355
aggcactcag	gctgtcctcg	gggaagatga	tcccagaaac	gttccggaag	ggactgtaat	3415
caaatggaca	aaagtctctg	ggaacgcgtg	caagatgaag	gcggccgatg	tctgctcttc	3475
gcctaactat	tgctttcatg	atttaattta	cgacggagga	aagaaagact	gcccgcgccg	3535
gggacccctg	tctgcaaacc	tggtaathtt	actaaagcgc	ggcgaaagct	tcccgggtta	3595
attaacgtac						3605

```
<210> 4
<211> 434
<212> PRT
<213> Infectious Laryngotracheitis Virus
```

<400>	4															
Met	His	Arg	Pro	His	Leu	Arg	Arg	His	Ser	Arg	Tyr	Tyr	Ala	Lys	Gly	
1				5					10					15		
Glu	Val	Leu	Asn	Lys	His	Met	Asp	Cys	Gly	Gly	Lys	Arg	Cys	Cys	Ser	
			20					25					30			
Gly	Ala	Ala	Val	Phe	Thr	Leu	Phe	Trp	Thr	Cys	Val	Arg	Ile	Met	Arg	
		35					40					45				
Glu	His	Ile	Cys	Phe	Val	Arg	Asn	Ala	Met	Asp	Arg	His	Leu	Phe	Leu	
	50					55					60					
Arg	Asn	Ala	Phe	Trp	Thr	Ile	Val	Leu	Leu	Ser	Ser	Phe	Ala	Ser	Gln	
65					70					75					80	
Ser	Thr	Ala	Ala	Val	Thr	Tyr	Asp	Tyr	Ile	Leu	Gly	Arg	Arg	Ala	Leu	
				85					90					95		
Asp	Ala	Leu	Thr	Ile	Pro	Ala	Val	Gly	Pro	Tyr	Asn	Arg	Tyr	Leu	Thr	
			100					105					110			
Arg	Val	Ser	Arg	Gly	Cys	Asp	Val	Val	Glu	Leu	Asn	Pro	Ile	Ser	Asn	
		115					120					125				
Val	Asp	Asp	Met	Ile	Ser	Ala	Ala	Lys	Glu	Lys	Glu	Lys	Gly	Gly	Pro	
	130					135					140					
Phe	Glu	Ala	Ser	Val	Val	Trp	Phe	Tyr	Val	Ile	Lys	Gly	Asp	Asp	Gly	
145				150						155					160	
Glu	Asp	Lys	Tyr	Cys	Pro	Ile	Tyr	Arg	Lys	Glu	Tyr	Arg	Glu	Cys	Gly	
				165					170					175		
Asp	Val	Gln	Leu	Leu	Ser	Glu	Cys	Ala	Val	Gln	Ser	Ala	Gln	Met	Trp	
		180					185					190				

Ala Val Asp Tyr Val Pro Ser Thr Leu Val Ser Arg Asn Gly Ala Gly
 195 200 205
 Leu Thr Ile Phe Ser Pro Thr Ala Ala Leu Ser Gly Gln Tyr Leu Leu
 210 215 220
 Thr Leu Lys Ile Gly Arg Phe Ala Gln Thr Ala Leu Val Thr Leu Glu
 225 230 235 240
 Val Asn Asp Arg Cys Leu Lys Ile Gly Ser Gln Leu Asn Phe Leu Pro
 245 250 255
 Ser Lys Cys Trp Thr Thr Glu Gln Tyr Gln Thr Gly Phe Gln Gly Glu
 260 265 270
 His Leu Tyr Pro Ile Ala Asp Thr Asn Thr Arg His Ala Asp Asp Val
 275 280 285
 Tyr Arg Gly Tyr Glu Asp Ile Leu Gln Arg Trp Asn Asn Leu Leu Arg
 290 295 300
 Lys Lys Asn Pro Ser Ala Pro Asp Pro Arg Pro Asp Ser Val Pro Gln
 305 310 315 320
 Glu Ile Pro Ala Val Thr Lys Lys Ala Glu Gly Arg Thr Pro Asp Ala
 325 330 335
 Glu Ser Ser Glu Lys Lys Ala Pro Pro Glu Asp Ser Glu Asp Asp Met
 340 345 350
 Gln Ala Glu Ala Ser Gly Glu Asn Pro Ala Ala Leu Pro Glu Asp Asp
 355 360 365
 Glu Val Pro Glu Asp Thr Glu His Asp Asp Pro Asn Ser Asp Pro Asp
 370 375 380
 Tyr Tyr Asn Asp Met Pro Ala Val Ile Pro Val Glu Glu Thr Thr Lys
 385 390 395 400
 Ser Ser Asn Ala Val Ser Met Pro Ile Phe Ala Ala Phe Val Ala Cys
 405 410 415
 Ala Val Ala Leu Val Gly Leu Leu Val Trp Ser Ile Val Lys Cys Ala
 420 425 430
 Arg Ser

<210> 5
 <211> 362
 <212> PRT
 <213> Infectious Laryngotracheitis Virus

<400> 5
 Met Ala Ser Leu Leu Gly Thr Leu Ala Leu Leu Ala Ala Thr Leu Ala
 1 5 10 15
 Pro Phe Gly Ala Met Gly Ile Val Ile Thr Gly Asn His Val Ser Ala
 20 25 30
 Arg Ile Asp Asp Asp His Ile Val Ile Val Ala Pro Arg Pro Glu Ala
 35 40 45
 Thr Ile Gln Leu Gln Leu Phe Phe Met Pro Gly Gln Arg Pro His Lys
 50 55 60
 Pro Tyr Ser Gly Thr Val Arg Val Ala Phe Arg Ser Asp Ile Thr Asn
 65 70 75 80

Gln	Cys	Tyr	Gln	Glu 85	Leu	Ser	Glu	Glu	Arg 90	Phe	Glu	Asn	Cys	Thr 95	His
Arg	Ser	Ser	Ser 100	Val	Phe	Val	Gly	Cys 105	Lys	Val	Thr	Glu	Tyr 110	Thr	Phe
Ser	Ala	Ser 115	Asn	Arg	Leu	Thr	Gly 120	Pro	Pro	His	Pro	Phe 125	Lys	Leu	Thr
Ile	Arg 130	Asn	Pro	Arg	Pro	Asn 135	Asp	Ser	Gly	Met	Phe 140	Tyr	Val	Ile	Val
Arg 145	Leu	Asp	Asp	Thr	Lys 150	Glu	Pro	Ile	Asp	Val 155	Phe	Ala	Ile	Gln	Leu 160
Ser	Val	Tyr	Gln	Phe 165	Ala	Asn	Thr	Ala	Ala 170	Thr	Arg	Gly	Leu	Tyr 175	Ser
Lys	Ala	Ser	Cys 180	Arg	Thr	Phe	Gly	Leu 185	Pro	Thr	Val	Gln	Leu 190	Glu	Ala
Tyr	Leu	Arg 195	Thr	Glu	Glu	Ser	Trp 200	Arg	Asn	Trp	Gln	Ala 205	Tyr	Val	Ala
Thr	Glu 210	Ala	Thr	Thr	Thr	Ser 215	Ala	Glu	Ala	Thr	Thr 220	Pro	Thr	Pro	Val
Thr 225	Ala	Thr	Ser	Ala	Ser 230	Glu	Leu	Glu	Ala	Glu 235	His	Phe	Thr	Phe	Pro 240
Trp	Leu	Glu	Asn	Gly 245	Val	Asp	His	Tyr	Glu 250	Pro	Thr	Pro	Ala	Asn 255	Glu
Asn	Ser	Asn	Val 260	Thr	Val	Arg	Leu	Gly 265	Thr	Met	Ser	Pro	Thr 270	Leu	Ile
Gly	Val	Thr 275	Val	Ala	Ala	Val	Val 280	Ser	Ala	Thr	Ile	Gly 285	Leu	Val	Ile
Val	Ile 290	Ser	Ile	Val	Thr	Arg 295	Asn	Met	Cys	Thr	Pro 300	His	Arg	Lys	Leu
Asp 305	Thr	Val	Ser	Gln	Asp 310	Asp	Glu	Glu	Arg	Ser 315	Gln	Thr	Arg	Arg	Glu 320
Ser	Arg	Lys	Phe	Gly 325	Pro	Met	Val	Ala	Cys 330	Glu	Ile	Asn	Lys	Gly 335	Ala
Asp	Gln	Asp	Ser 340	Glu	Leu	Val	Glu	Leu 345	Val	Ala	Ile	Val	Asn 350	Pro	Ser
Ala	Leu	Ser 355	Ser	Pro	Asp	Ser	Ile 360	Lys	Met						